

# SEQUENCE LISTING

<110> Busfield, Samantha J.

<120> NOVEL MOLECULES OF THE  
HERPESVIRUS-ENTRY-MEDIATOR-RELATED  
PROTEIN FAMILY AND USES THEREOF

<130> MBIO98-061CP1

<150> US 09/146,950

<151> 1998-09-03

<160> 58

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1929

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (297) ... (875)

<400> 1

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cctgctgccc actctcctgc tgctcgggtt ctgaggcaca gcttgtcaca ccgaggcgga      180
ttctctttct ctttctcttt ctcttctggc ccacagccgc agcaatggcg ctgagttcct      240
ctgctggagt tcctcctgct agctgggttc ccgagctgcc ggtctgagcc tgaggc atg      299
                                         Met
                                         1

gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga      347
Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg
          5                      10                      15

acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc      395
Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro
          20                      25                      30

tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg      443
Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val
          35                      40                      45

ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag      491
Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu
          50                      55                      60

gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc      539
Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly
          70                      75                      80

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63246560

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<400> 2
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Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
      -20                      -15                      -10
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
      -5                      1                      5                      10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
      15                      20                      25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
      30                      35                      40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
      45                      50                      55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
      60                      65                      70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
      75                      80                      85                      90
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
      95                      100                      105
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
      110                      115                      120
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
      125                      130                      135
Glu Glu Cys Gln His Gln Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp
      140                      145                      150
Leu
155

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<210> 3
<211> 579
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)...(579)

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<400> 3
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  1                      5                      10                      15

aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc      96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
      20                      25                      30

ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca      144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
      35                      40                      45

gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag      192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
      50                      55                      60

gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca      240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
      65                      70                      75                      80

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ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc	288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	
85 90 95	

caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc	336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	
100 105 110	

agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc	384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	
115 120 125	

gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc	432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	
130 135 140	

agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc	480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	
145 150 155 160	

ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg	528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	
165 170 175	

gag gaa tgt cag cac cag acc aac cga gct tgg aaa agt cag aca gac	576
Glu Glu Cys Gln His Gln Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp	
180 185 190	

ctc	579
Leu	

<210> 4  
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 <212> PRT  
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<400> 4

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Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His	
35 40 45	
Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala	
50 55 60	
Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val	
65 70 75 80	
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His	
85 90 95	
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val	
100 105 110	
Gln Lys Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro	
115 120 125	
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln	

130 135 140  
 Thr Asn Arg Ala Trp Lys Ser Gln Thr Asp Leu  
 145 150 155

<210> 5  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(38)

<400> 5  
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 -20 -15 -10  
 Pro Cys Tyr Ala Pro Ala  
 -5

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 <212> DNA  
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 <220>  
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 <222> (1)...(114)

<400> 6  
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 aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96  
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
 20 25 30  
 ccc tgc tac gcc cca gct 114  
 Pro Cys Tyr Ala Pro Ala  
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<210> 7  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<400> 7  
 Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys  
 1 5 10 15  
 Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr  
 20 25 30  
 Val Cys

<210> 8  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys  
 1 5 10 15  
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg  
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 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys  
 35 40

<210> 9  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 9  
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala  
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 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys  
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 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys  
 35 40

<210> 10  
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 <212> DNA  
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<220>  
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 <222> (1)...(105)

<400> 10  
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 Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys  
 1 5 10 15  
 tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc 96  
 Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly  
 20 25 30  
 aca gtg tgt 105  
 Thr Val Cys  
 35

<210> 11  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(126)

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<400> 11
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Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys
 1          5          10          15

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg      96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg
          20          25          30

aac tgc tcc agg aca gag aac gcc gtg tgt      126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys
          35          40

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<210> 12
<211> 126
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)...(126)

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<400> 12
tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc      48
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala
 1          5          10          15

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag      96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
          20          25          30

gga ggc acc gag agt cag gac acc ctg tgt      126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
          35          40

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<210> 13
<211> 283
<212> PRT
<213> Homo sapiens

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<220>
<221> SIGNAL
<222> (1)...(38)

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Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
          -20          -15          -10
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
          -5          1          5          10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
          15          20          25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro

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			30					35					40				
Gly	Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys		
			45					50					55				
Gln	Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser		
			60					65					70				
Arg	Thr	Glu	Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile		
			75					80					85				
Val	Gln	Asp	Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser		
			95					100					105				
Ser	Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr		
			110					115					120				
Leu	Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu		
			125					130					135				
Glu	Glu	Cys	Gln	His	Gln	Thr	Lys	Cys	Ser	Trp	Leu	Val	Thr	Lys	Ala		
			140					145					150				
Gly	Ala	Gly	Thr	Ser	Ser	Ser	His	Trp	Val	Trp	Trp	Phe	Leu	Ser	Gly		
			155					160					165				
Ser	Leu	Val	Ile	Val	Ile	Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys		
			175					180					185				
Val	Lys	Arg	Arg	Lys	Pro	Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser		
			190					195					200				
Val	Gln	Arg	Lys	Arg	Gln	Glu	Ala	Glu	Gly	Glu	Ala	Thr	Val	Ile	Glu		
			205					210					215				
Ala	Leu	Gln	Ala	Pro	Pro	Asp	Val	Thr	Thr	Val	Ala	Val	Glu	Glu	Thr		
			220					225					230				
Ile	Pro	Ser	Phe	Thr	Gly	Arg	Ser	Pro	Asn	His							
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<210> 14
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<212> DNA
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<221> CDS
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ccccctgctg	cccactctcc	tgctgctcgg	gttctgaggc	acagcttgtc	acaccgagggc	180
ggattctctt	tctctttctc	ttctggccca	cagccgcagc	aatggcgctg	agttcctctg	240
ctggagttca	tctgctagc	tgggttcccc	agctgccggt	ctgagcctga	ggc atg	296
				Met		
				1		



ggc	tcc	gag	tgc	tgc	ccc	aag	tgc	agt	cca	ggt	tat	cgt	gtg	aag	gag	488
Gly	Ser	Glu	Cys	Cys	Pro	Lys	Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	
50					55					60					65	
gcc	tgc	ggg	gag	ctg	acg	ggc	aca	gtg	tgt	gaa	ccc	tgc	cct	cca	ggc	536
Ala	Cys	Gly	Glu	Leu	Thr	Gly	Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	
				70					75					80		
acc	tac	att	gcc	cac	ctc	aat	ggc	cta	agc	aag	tgt	ctg	cag	tgc	caa	584
Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	
			85					90					95			
atg	tgt	gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	aac	tgc	tcc	agg	632
Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	Asn	Cys	Ser	Arg	
		100					105					110				
aca	gag	aac	gcc	gtg	tgt	ggc	tgc	agc	cca	ggc	cac	ttc	tgc	atc	gtc	680
Thr	Glu	Asn	Ala	Val	Cys	Gly	Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	
	115					120					125					
cag	gac	ggg	gac	cac	tgc	gcc	gcg	tgc	cgc	gct	tac	gcc	acc	tcc	agc	728
Gln	Asp	Gly	Asp	His	Cys	Ala	Ala	Cys	Arg	Ala	Tyr	Ala	Thr	Ser	Ser	
130					135					140					145	
ccg	ggc	cag	agg	gtg	cag	aag	gga	ggc	acc	gag	agt	cag	gac	acc	ctg	776
Pro	Gly	Gln	Arg	Val	Gln	Lys	Gly	Gly	Thr	Glu	Ser	Gln	Asp	Thr	Leu	
				150					155					160		
tgt	cag	aac	tgc	ccc	ccg	ggg	acc	ttc	tct	ccc	aat	ggg	acc	ctg	gag	824
Cys	Gln	Asn	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Pro	Asn	Gly	Thr	Leu	Glu	
			165					170					175			
gaa	tgt	cag	cac	cag	acc	aag	tgc	agc	tgg	ctg	gtg	acg	aag	gcc	gga	872
Glu	Cys	Gln	His	Gln	Thr	Lys	Cys	Ser	Trp	Leu	Val	Thr	Lys	Ala	Gly	
		180					185					190				
gct	ggg	acc	agc	agc	tcc	cac	tgg	gta	tgg	tgg	ttt	ctc	tca	ggg	agc	920
Ala	Gly	Thr	Ser	Ser	Ser	His	Trp	Val	Trp	Trp	Phe	Leu	Ser	Gly	Ser	
	195					200					205					
ctc	gtc	atc	gtc	att	gtt	tgc	tcc	aca	gtt	ggc	cta	atc	ata	tgt	gtg	968
Leu	Val	Ile	Val	Ile	Val	Cys	Ser	Thr	Val	Gly	Leu	Ile	Ile	Cys	Val	
210					215					220					225	
aaa	aga	aga	aag	cca	agg	ggt	gat	gta	gtc	aag	gtg	atc	gtc	tcc	gtc	1016
Lys	Arg	Arg	Lys	Pro	Arg	Gly	Asp	Val	Val	Lys	Val	Ile	Val	Ser	Val	
				230					235					240		
cag	cgg	aaa	aga	cag	gag	gca	gaa	ggt	gag	gcc	aca	gtc	att	gag	gcc	1064
Gln	Arg	Lys	Arg	Gln	Glu	Ala	Glu	Gly	Glu	Ala	Thr	Val	Ile	Glu	Ala	
			245					250					255			
ctg	cag	gcc	cct													

ccc tca ttc acg ggg agg agc cca aac cac tgacccacag actctgcacc 1162  
 Pro Ser Phe Thr Gly Arg Ser Pro Asn His  
 275 280

ccgacgccag agatacctgg agcgacggct gctgaaagag gctgtccacc tggcgaaacc 1222  
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 ggagaggtgg ggcccctgct ggggtagagc tggggacgcc acgtgccatt cccatggggc 1342  
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<400> 15  
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<400> 16  
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<210> 17  
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<220>  
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 <222> (107)...(697)

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 Met Glu Pro  
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cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac 163  
 Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp  
 5 10 15

gtc ttg agg ctg gtg ctg tat ctc acc ttt ctg gga gcc ccc tgc tac 211  
 Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr  
 20 25 30 35

gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg ggc tcc 259  
 Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser  
 40 45 50

gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag gcc tgc	307
Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys	
55 60 65	
ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc acc tac	355
Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr	
70 75 80	
att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa atg tgt	403
Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys	
85 90 95	
gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg aca gag	451
Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu	
100 105 110 115	
aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc cag gac	499
Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp	
120 125 130	
ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc ccg ggc	547
Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly	
135 140 145	
cag agg gtg cag aag gga ggc acc gag agt cag gac acc ctg tgt cag	595
Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln	
150 155 160	
aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg gag gaa tgt	643
Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys	
165 170 175	
cag cac cag acc aat tgg cct aat cat atg tgt gaa aag aag aaa gcc	691
Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys Lys Lys Ala	
180 185 190 195	
aag ggg tgagcacacg gcggcccat caggggtcat gtccccagcc gtcacctctt	747
Lys Gly	
ggagctctgt caccceaagc ctgggaggtg gccccagagc ttttccagga tccgcggctc	807
ctcccagggc agccactgca ggctggggca ggtgatgtag tcaaggtgat cgtctccatc	867
cagcggaaaa gacaggaggc agaaggtgag gccacagtca ttgaggccct gcaggccct	927
ccggacgtca ccacggtggc cgtggaggag acaataccct cattcacggg gaggagccca	987
aaccactgac ccacagactc tgcaccccgga cgccagagat acctggagcg acggctgctg	1047
aaagaggctg tccacctggc gaaaccaccg gagcccggag gcttgggggc tccgccctgg	1107
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gacgccacgt gccattccca tgggcagtg agggcctggg gcctctgttc tgcgtggcc	1227
tgagctcccc agagtccctga ggaggagcgc cagttgcccc tcgctcacag accacacacc	1287
cagccctcct gggccagccc agagggccct tcagacccca gctgtctgcg cgtctgactc	1347
ttgtggcctc agcaggacag gccccgggca ctgcctcaca gccaaggctg gactgggttg	1407
gctgcagtg ggtgtttagt ggataccaca tcggaagtga ttttctaaat tggatttgaa	1467
ttcggctcct gttttctatt tgcattgaaa cagtgtatctt ggggagatgc tgtgggagga	1527
tgtaaatatc ttgtttctcc tcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1587
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<210> 18  
 <211> 197  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(38)

<400> 18

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
 -35 -30 -25  
 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
 -20 -15 -10  
 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro  
 -5 1 5 10  
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys  
 15 20 25  
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro  
 30 35 40  
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys  
 45 50 55  
 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser  
 60 65 70  
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile  
 75 80 85 90  
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser  
 95 100 105  
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr  
 110 115 120  
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu  
 125 130 135  
 Glu Glu Cys Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys  
 140 145 150  
 Lys Lys Ala Lys Gly  
 155

<210> 19  
 <211> 591  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(591)

<400> 19

atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc	48
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro	
1 5 10 15	
aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttt ctg gga gcc	96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	
20 25 30	
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca	144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro	

35	40	45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag			192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys			
50	55	60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca			240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro			
65	70	75	80
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc			288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys			
85	90	95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc			336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser			
100	105	110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc			384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile			
115	120	125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc			432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser			
130	135	140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc			480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr			
145	150	155	160
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg			528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu			
165	170	175	
gag gaa tgt cag cac cag acc aat tgg cct aat cat atg tgt gaa aag			576
Glu Glu Cys Gln His Gln Thr Asn Trp Pro Asn His Met Cys Glu Lys			
180	185	190	
aag aaa gcc aag ggg			591
Lys Lys Ala Lys Gly			
195			

<210> 20  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys  
 1 5 10 15  
 Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu  
 20 25 30  
 Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His  
 35 40 45  
 Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala  
 50 55 60

Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val  
65 70 75 80  
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His  
85 90 95  
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val  
100 105 110  
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro  
115 120 125  
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln  
130 135 140  
Thr Asn Trp Pro Asn His Met Cys Glu Lys Lys Lys Ala Lys Gly  
145 150 155

<210> 21  
<211> 38  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SIGNAL  
<222> (1)...(38)

<400> 21  
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-35 -30 -25  
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
-20 -15 -10  
Pro Cys Tyr Ala Pro Ala  
-5

<210> 22  
<211> 114  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(114)

<400> 22  
atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48  
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
1 5 10 15  
aga acc gac gtc tcg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96  
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
20 25 30  
ccc tgc tac gcc cca gct 114  
Pro Cys Tyr Ala Pro Ala  
35

<210> 23  
<211> 34  
<212> PRT  
<213> Homo sapiens

[illegible]

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<210> 24
<211> 42
<212> PRT
<213> Homo sapiens
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<210> 25
<211> 42
<212> PRT
<213> Homo sapiens
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<210> 26
<211> 105
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> (1)...(105)
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15

<210> 27  
 <211> 126  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(126)

<400> 27

tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt 48  
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys  
 1 5 10 15

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg 96  
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg  
 20 25 30

aac tgc tcc agg aca gag aac gcc gtg tgt 126  
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys  
 35 40

<210> 28  
 <211> 126  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(126)

<400> 28

tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc 48  
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala  
 1 5 10 15

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag 96  
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys  
 20 25 30

gga ggc acc gag agt cag gac acc ctg tgt 126  
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys  
 35 40

<210> 29  
 <211> 2313  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (85)...(642)

<400> 29



gtcgacccac gcgtccggt gagttcctct gctggagttc atcctgctag ctgggttccc	60
gagctgccgg tctgagcctg aggc atg gag cct cct gga gac tgg ggg cct	111
Met Glu Pro Pro Gly Asp Trp Gly Pro	
1 5	
cct ccc tgg aga tcc acc ccc aga acc gac gtc tgc agg ctg gtg ctg	159
Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val Ser Arg Leu Val Leu	
10 15 20 25	
tat ctc acc ttc ctg gga gcc ccc tgc tac gcc cca gct ctg ccg tcc	207
Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala Pro Ala Leu Pro Ser	
30 35 40	
tgc aag gag gac gag tac cca gtg ggc tcc gag tgc tgc ccc aag tgc	255
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys	
45 50 55	
agt cca ggt tat cgt gtg aag gag gcc tgc ggg gag ctg acg ggc aca	303
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr	
60 65 70	
gtg tgt gaa ccc tgc cct cca ggc acc tac att gcc cac ctc aat ggc	351
Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly	
75 80 85	
cta agc aag tgt ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg	399
Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu	
90 95 100 105	
cgc gcg agc cgg aac tgc tcc agg aca gag aac gcc gtg tgt ggc tgc	447
Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val Cys Gly Cys	
110 115 120	
agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc gcg	495
Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala Ala	
125 130 135	
tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag gga	543
Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys Gly	
140 145 150	
ggc acc gag agt cag gac acc ctg tgt cag aac tgc ccc ccg ggg acc	591
Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro Pro Gly Thr	
155 160 165	
ttc tct ccc aat ggg acc ctg gag gaa tgt cag cac cag acc aaa aag	639
Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln Thr Lys Lys	
170 175 180 185	
gct tgaagggtccc accctgagcg gcaccctggt cacatgcctg cgtccaggag	692
Ala	
agctgcaggg ctgaagcctg tgtgccccag ataaccctt ccatgggccc agacaaagcc	752
tcatcagatc tgagcttccct ggaggtccag gatgggcctt cccagaagca ggcccagagg	812
gaggctgcct ccagatcccc tgtccccctgg ggctgtgggt gtccctgaat gtcagggcca	872
tgggagggcc cctgggcttc aggggttggg gaaagtgaac actctgctct ttgtccacct	932

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tcgggaggac accttcaaat gctgacctg gggccctaac tgacctgaga cttcagagct 992
tcttggggagg agctgggggtc cccagcgga gctgggatg gagcaggat ggctgcccc 1052
gggaggggggc ggtggggcct tccatcctgc tctgcccctc tctcctctg gcccagctc 1112
agtctgttc atctccagct ctaaccattt ttgtcccgac actggctctc cctctacctt 1172
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cattgtttgc tccacagtgt gcctaatacat atgtgtgaaa agaagaaagc caaggggtga 1652
tgtagtcaag gtgatcgtct ccgtccagcg gaaaagacag gaggcagaag gtgaggccac 1712
agtcattgag gccctgcagg cccctccgga cgtcaccacg gtggcctggt aggagacaat 1772
acctcattc acggggaggga gcccaccca ctgaccaca gactctgcac cccgacgcca 1832
gagatacctg gagcgacggc tgctgaaaga ggctgtccac ctggcgaaac caccggagcc 1892
cggaggtctg ggggtccgc cctgggctgg cttcctctc ctccagtga gggagaggtg 1952
gggcccctgc tgggtagag ctggggacgc cactgcccac tcccatgggc cagtggggc 2012
ctggggcctc tgttctgctg tggcctgagc tcccagagt cctgaggagg agcgccagt 2072
ggccctcgtc cacagaccac acaccagcc ctctgggccc agccagagg gcccttcaga 2132
ccccagctgt ctgcgcgtct gactcttgtg gcctcagcag gacaggcccc gggcactgcc 2192
tcacagccaa ggctggactg ggttggtctg agtgtggtgt ttagtgata ccacatcgga 2252
agtgattttc taaattggat ttgaattcgg aaaaaaaaaa aaaaaaaaaa agggcggccg 2312
c 2313

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<210> 30  
 <211> 186  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(38)

<400> 30

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Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
-35 -30 -25
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
-20 -15 -10
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
-5 1 5 10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
15 20 25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
30 35 40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
45 50 55
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
60 65 70
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
75 80 85 90
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
95 100 105
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
110 115 120
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
125 130 135

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Glu Glu Cys Gln His Gln Thr Lys Lys Ala  
 140 145

<210> 31  
 <211> 558  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(558)

<400> 31

atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc	48
Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro	
1 5 10 15	
aga acc gac gtc tgc agg ctg gtg ctg tat ctc acc ttc ctg gga gcc	96
Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	
20 25 30	
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca	144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro	
35 40 45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag	192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys	
50 55 60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca	240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro	
65 70 75 80	
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc	288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	
85 90 95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc	336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	
100 105 110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc	384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	
115 120 125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc	432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	
130 135 140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc	480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	
145 150 155 160	
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg	528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	
165 170 175	

gag gaa tgt cag cac cag acc aaa aag gct  
 Glu Glu Cys Gln His Gln Thr Lys Lys Ala  
 180 185

558

<210> 32  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 32

Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys  
 1 5 10 15  
 Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu  
 20 25 30  
 Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His  
 35 40 45  
 Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala  
 50 55 60  
 Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val  
 65 70 75 80  
 Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His  
 85 90 95  
 Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val  
 100 105 110  
 Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro  
 115 120 125  
 Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln  
 130 135 140  
 Thr Lys Lys Ala  
 145

<210> 33  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(38)

<400> 33

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
 -35 -30 -25  
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
 -20 -15 -10  
 Pro Cys Tyr Ala Pro Ala  
 -5

<210> 34  
 <211> 114  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(114)

<400> 34  
 atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc 48  
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
 1 5 10 15  
  
 aga acc gac gtc tgc agg ctg gtg ctg tat ctc acc ttc ctg gga gcc 96  
 Arg Thr Asp Val Ser Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
 20 25 30  
  
 ccc tgc tac gcc cca gct 114  
 Pro Cys Tyr Ala Pro Ala  
 35

<210> 35  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<400> 35  
 Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys  
 1 5 10 15  
 Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr  
 20 25 30  
 Val Cys

<210> 36  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys  
 1 5 10 15  
 Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg  
 20 25 30  
 Asn Cys Ser Arg Thr Glu Asn Ala Val Cys  
 35 40

<210> 37  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 37  
 Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala  
 1 5 10 15  
 Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys  
 20 25 30  
 Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys  
 35 40

<210> 38  
 <211> 105  
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(105)

<400> 38

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Ser	Cys	Lys	Glu	Asp	Glu	Tyr	Pro	Val	Gly	Ser	Glu	Cys	Cys	Pro	Lys	
1				5					10					15		

tgc	agt	cca	ggg	tat	cgt	gtg	aag	gag	gcc	tgc	ggg	gag	ctg	acg	ggc	96
Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	Ala	Cys	Gly	Glu	Leu	Thr	Gly	
			20					25					30			

aca	gtg	tgt														105
Thr	Val	Cys														
			35													

<210> 39

<211> 126

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(126)

<400> 39

tgc	cct	cca	ggc	acc	tac	att	gcc	cac	ctc	aat	ggc	cta	agc	aag	tgt	48
Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His	Leu	Asn	Gly	Leu	Ser	Lys	Cys	
1				5					10					15		

ctg	cag	tgc	caa	atg	tgt	gac	cca	gcc	atg	ggc	ctg	cgc	gcg	agc	cgg	96
Leu	Gln	Cys	Gln	Met	Cys	Asp	Pro	Ala	Met	Gly	Leu	Arg	Ala	Ser	Arg	
			20					25					30			

aac	tgc	tcc	agg	aca	gag	aac	gcc	gtg	tgt							126
Asn	Cys	Ser	Arg	Thr	Glu	Asn	Ala	Val	Cys							
			35					40								

<210> 40

<211> 126

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(126)

<400> 40

tgc	agc	cca	ggc	cac	ttc	tgc	atc	gtc	cag	gac	ggg	gac	cac	tgc	gcc	48
Cys	Ser	Pro	Gly	His	Phe	Cys	Ile	Val	Gln	Asp	Gly	Asp	His	Cys	Ala	
1				5					10					15		

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gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag      96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys
      20              25              30

gga ggc acc gag agt cag gac acc ctg tgt      126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys
      35              40

<210> 41
<211> 1834
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (103)...(933)

<400> 41
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cctgctagct gggttcccga gctgccggtc tgagcctgag gc atg gag cct cct      114
                               Met Glu Pro Pro
                               1

gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc aga acc gac gtc      162
Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro Arg Thr Asp Val
  5              10              15              20

ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc ccc tgc tac gcc      210
Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala
      25              30              35

cca gct ctg ccg tcc tgc aag gag gac gag tac cca gtg ggc tcc gag      258
Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu
      40              45              50

tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag gag gcc tgc ggg      306
Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly
      55              60              65

gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca ggc acc tac att      354
Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile
      70              75              80

gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc caa atg tgt gac      402
Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp
      85              90              95              100

cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc agg aca gag aac      450
Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn
      105              110              115

gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg      498
Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly
      120              125              130

gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag      546

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Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln	
135 140 145	
agg gtg cag aag gga ggc acc gag agt cag gac acc ctg tgt cag aac	594
Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn	
150 155 160	
tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg gag gaa tgt cag	642
Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln	
165 170 175 180	
cac cag acc aag tgc agc tgg ctg gtg acg aag gcc gga gct ggg acc	690
His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly Ala Gly Thr	
185 190 195	
agc agc tcc cac tgg gta tgg tgg ttt ctc tca ggg agc ctc gtc atc	738
Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile	
200 205 210	
gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt gtg aaa aga aga	786
Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys Val Lys Arg Arg	
215 220 225	
aag cca agg ggt gat gta gtc aag gtg atc gtc tcc gtc cag gta ttg	834
Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser Val Gln Val Leu	
230 235 240	
atc ctc ctc ccc ctc tcc ctc ccc cct cca cct tcc cac ctc ccc tct	882
Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Pro Ser His Leu Pro Ser	
245 250 255 260	
ccc cgc tgg ggc tgg tgt ttc tgg tgt aca tgg tgg ggg ctc cca gtt	930
Pro Arg Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp Gly Leu Pro Val	
265 270 275	
ctc tgagggtcct gagtctttca agtacagcca cggtagctca ggaaagaacc	983
Leu	
cacccccctca aactgaaagc agtaaaatga acccgagaac ctggagtccc agggggggcct	1043
gagcaggcag ggtctccacg attcgtgtgc tcacagcgga aaagacagga ggcagaaggt	1103
gaggccacag tcattgaggc cctgcaggcc cctccggacg tcaccacggg ggccgtggag	1163
gagacaatac cctcattcac ggggaggagc ccaaaccact gacccacaga ctctgcaccc	1223
cgacgccaga gatacctgga gcgacggctg ctgaaagagg ctgtccacct ggcgaaacca	1283
ccggagcccc gaggtttggg ggctccgccc tgggctggct tccgtctcct ccagtggagg	1343
gagaggtggg gcccctgctg gggtagagct ggggacgcca cgtgccattc ccatgggcca	1403
gtgagggcct ggggcctctg ttctgctgtg gcctgagctc cccagagtcc tgaggaggag	1463
cgccagttgc cctcgtctca cagaccacac acccagccct cctgggccag cccagagggc	1523
ccttcagacc ccagctgtct gcgcgtctga ctcttgtggc ctcagcagga caggccccgg	1583
gcaactgcctc acagccaagg ctggactggg ttggctgcag tgtggtgttt agtggatacc	1643
acatcggaag tgattttcta aattggattt gaattcggct cctgttttct atttgtcatg	1703
aaacagtgtg tttggggaga tgctgtggga ggatgtaaat atcttgtttc tcctcaaaaa	1763
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1823
agggcggccg c	1834

<210> 42  
<211> 277



<212> PRT  
 <213> Homo sapiens

<220>  
 <221> SIGNAL  
 <222> (1)...(38)

<400> 42

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro  
 -35 -30 -25  
 Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala  
 -20 -15 -10  
 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro  
 -5 1 5 10  
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys  
 15 20 25  
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro  
 30 35 40  
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys  
 45 50 55  
 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser  
 60 65 70  
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile  
 75 80 85 90  
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser  
 95 100 105  
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr  
 110 115 120  
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu  
 125 130 135  
 Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala  
 140 145 150  
 Gly Ala Gly Thr Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly  
 155 160 165 170  
 Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys  
 175 180 185  
 Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser  
 190 195 200  
 Val Gln Val Leu Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Pro Ser  
 205 210 215  
 His Leu Pro Ser Pro Arg Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp  
 220 225 230  
 Gly Leu Pro Val Leu  
 235

<210> 43  
 <211> 831  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(831)

<400> 43

atg gag cct cct gga gac tgg ggg cct cct ccc tgg aga tcc acc ccc  
 Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro

48

1	5	10	15	
aga acc gac gtc ttg agg ctg gtg ctg tat ctc acc ttc ctg gga gcc				96
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala	20	25	30	
ccc tgc tac gcc cca gct ctg ccg tcc tgc aag gag gac gag tac cca				144
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro	35	40	45	
gtg ggc tcc gag tgc tgc ccc aag tgc agt cca ggt tat cgt gtg aag				192
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys	50	55	60	
gag gcc tgc ggg gag ctg acg ggc aca gtg tgt gaa ccc tgc cct cca				240
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro	65	70	75	80
ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt ctg cag tgc				288
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys	85	90	95	
caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg aac tgc tcc				336
Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser	100	105	110	
agg aca gag aac gcc gtg tgt ggc tgc agc cca ggc cac ttc tgc atc				384
Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile	115	120	125	
gtc cag gac ggg gac cac tgc gcc gcg tgc cgc gct tac gcc acc tcc				432
Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser	130	135	140	
agc ccg ggc cag agg gtg cag aag gga ggc acc gag agt cag gac acc				480
Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr	145	150	155	160
ctg tgt cag aac tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg				528
Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu	165	170	175	
gag gaa tgt cag cac cag acc aag tgc agc tgg ctg gtg acg aag gcc				576
Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala	180	185	190	
gga gct ggg acc agc agc tcc cac tgg gta tgg tgg ttt ctc tca ggg				624
Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly	195	200	205	
agc ctc gtc atc gtc att gtt tgc tcc aca gtt ggc cta atc ata tgt				672
Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys	210	215	220	
gtg aaa aga aga aag cca agg ggt gat gta gtc aag gtg atc gtc tcc				720
Val Lys Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser	225	230	235	240

gtc cag gta ttg atc ctc ctc ccc ctc tcc ctc ccc cct cca cct tcc	768
Val Gln Val Leu Ile Leu Leu Pro Leu Ser Leu Pro Pro Pro Pro Ser	
245 250 255	
cac ctc ccc tct ccc cgc tgg ggc tgg tgt ttc tgg tgt aca tgg tgg	816
His Leu Pro Ser Pro Arg Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp	
260 265 270	
ggg ctc cca gtt ctc	831
Gly Leu Pro Val Leu	
275	

<210> 44  
 <211> 239  
 <212> PRT  
 <213> Homo sapiens

<400> 44

Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys	
1 5 10 15	
Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu	
20 25 30	
Thr Gly Thr Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His	
35 40 45	
Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala	
50 55 60	
Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val	
65 70 75 80	
Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His	
85 90 95	
Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val	
100 105 110	
Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro	
115 120 125	
Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln	
130 135 140	
Thr Lys Cys Ser Trp Leu Val Thr Lys Ala Gly Ala Gly Thr Ser Ser	
145 150 155 160	
Ser His Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile Val Ile	
165 170 175	
Val Cys Ser Thr Val Gly Leu Ile Ile Cys Val Lys Arg Arg Lys Pro	
180 185 190	
Arg Gly Asp Val Val Lys Val Ile Val Ser Val Gln Val Leu Ile Leu	
195 200 205	
Leu Pro Leu Ser Leu Pro Pro Pro Ser His Leu Pro Ser Pro Arg	
210 215 220	
Trp Gly Trp Cys Phe Trp Cys Thr Trp Trp Gly Leu Pro Val Leu	
225 230 235	

<210> 45  
 <211> 38  
 <212> PRT  
 <213> Homo sapiens

<220>





Thr Val Cys  
35

<210> 53  
<211> 126  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(126)

<400> 53

tgc cct cca ggc acc tac att gcc cac ctc aat ggc cta agc aag tgt	48
Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys	
1 5 10 15	

ctg cag tgc caa atg tgt gac cca gcc atg ggc ctg cgc gcg agc cgg	96
Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg	
20 25 30	

aac tgc tcc agg aca gag aac gcc gtg tgt	126
Asn Cys Ser Arg Thr Glu Asn Ala Val Cys	
35 40	

<210> 54  
<211> 126  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(126)

<400> 54

tgc agc cca ggc cac ttc tgc atc gtc cag gac ggg gac cac tgc gcc	48
Cys Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala	
1 5 10 15	

gcg tgc cgc gct tac gcc acc tcc agc ccg ggc cag agg gtg cag aag	96
Ala Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys	
20 25 30	

gga ggc acc gag agt cag gac acc ctg tgt	126
Gly Gly Thr Glu Ser Gln Asp Thr Leu Cys	
35 40	

<210> 55  
<211> 66  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS

<222> (1)...(66)

<400> 55

tgc ccc ccg ggg acc ttc tct ccc aat ggg acc ctg gag gaa tgt cag 48  
Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln  
1 5 10 15

cac cag acc aag tgc agc 66  
His Gln Thr Lys Cys Ser  
20

<210> 56

<211> 75

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(75)

<400> 56

tgg gta tgg tgg ttt ctc tca ggg agc ctc gtc atc gtc att gtt tgc 48  
Trp Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile Val Ile Val Cys  
5 10 15

tgc aca gtt ggc cta atc ata tgt gtg 75  
Ser Thr Val Gly Leu Ile Ile Cys Val  
20 25

<210> 57

<211> 32

<212> DNA

<213> Homo sapiens

<220>

<400> 57

tttttctcga ggccatggag cctcctggag ac 32

<210> 58

<211> 39

<212> DNA

<213> Homo sapiens

<220>

<400> 58

tttttggtatc cgctgctgag aggtctgtct gacttttcc 39